What is claimed is:

1. A substantially pure PAMP nucleic acid molecule comprising a nucleic acid sequence encoding substantially a PAMP polypeptide.

2. The substantially pure PAMP nucleic acid molecule of claim 1, which encodes the amino acid sequence shown as SEQ ID NO:2.

3. The substantially pure PAMP nucleic acid molecule of claim 2, comprising the nucleotide sequence shown as SEQ ID NO:1.

4. A substantially pure PAMP nucleic acid probe, comprising substantially the nucleotide sequence of nucleotides 1 to 3221 of SEQ ID NO:1, or a fragment thereof, provided said probe does not have the nucleotide sequence of AA363808, AW959484, BE165930, nucleotides 1 to 614 of BE893201, or nucleotides 1 to 1530 of AK026780.

5. A substantially pure PAMP nucleic acid probe, comprising at least 10 contiguous nucleotides of SEQ ID NO:1, said contiguous nucleotides including at least one nucleotide of the nucleotide sequence shown as position 1 to position 3221 of SEQ ID NO:1, provided said probe does not have the nucleotide sequence of AA363808, AW959484, BE165930, nucleotides 1 to 614 of BE893201, or nucleotides 1 to 1530 of AK026780.

6. The substantially pure PAMP nucleic acid probe of claim 5, comprising at least 15 contiguous nucleotides of SEQ ID NO:1.

7. The substantially pure PAMP nucleic acid probe of claim 6, which is 15 to 18 nucleotides in length.

8. The substantially pure PAMP nucleic acid probe of claims 4, 5, 6 or 7, further comprising a detectable label.

9. A substantially pure PAMP polypeptide, comprising substantially the amino acid sequence shown as SEQ ID NO:2.

10. The substantially pure PAMP polypeptide of claim 9, comprising the amino acid sequence shown as SEQ ID NO:2.

11. A substantially pure PAMP polypeptide fragment, comprising at least eight contiguous amino acids of residues 1 to 1074 of SEQ ID NO:2.

12. The substantially pure PAMP polypeptide fragment of claim 11, comprising at least ten contiguous amino acids of residues 1 to 1074 of SEQ ID NO:2.

13. A method of diagnosing or predicting susceptibility to a prostate neoplastic condition in an individual, comprising:

(a) obtaining a sample from said individual;

(b) measuring a test expression level of PAMP RNA by hybridization with a PAMP nucleic acid probe comprising at least 10 contiguous nucleotides of SEQ ID NO:1, said contiguous nucleotides including at least one nucleotide of the nucleotide sequence shown as position 1 to position 3221 of SEQ ID NO:1 in said sample; and

(c) comparing said test expression level of PAMP RNA to a control expression level of PAMP RNA,

wherein a test expression level 2-fold or more greater than said control expression level indicates the presence of a prostate neoplastic condition.

14. The method of claim 13, wherein said sample comprises a prostate cell.

15. The method of claim 13, wherein said sample comprises prostate tissue.

16. The method of claim 13, wherein said control expression level is determined using a normal prostate cell or an androgen-dependent cell line.

17. The method of claim 13, wherein said sample is a fluid selected from the group consisting of blood, serum, urine and semen.

18. The method of claim 13, wherein said PAMP nucleic acid probe comprises at least 10 contiguous nucleotides of SEQ ID NO:1, said contiguous nucleotides including at least one nucleotide of the nucleotide sequence shown as position 1 to position 3221 of SEQ ID NO:1, provided said probe does not have the nucleotide sequence of AA363808, AW959484, BE165930, nucleotides 1 to 614 of BE893201 or nucleotides 1 to 1530 of AK026780.

19. The method of claim 13, wherein said PAMP nucleic acid probe is 15 to 18 nucleotides in length.

20. The method of claims 18 or 19, wherein said PAMP nucleic acid probe further comprises a detectable label.

21. A method of diagnosing or predicting susceptibility to a prostate neoplastic condition in an individual, comprising:

(a) obtaining a sample from said individual;

(b) measuring a test expression level of PAMP polypeptide by contacting a cell, a cell lysate, or fractionated sample thereof, from said individual with a binding agent selective for PAMP polypeptide residues 1 to 1074 of SEQ ID NO:2, and determining the amount of selective binding of said agent; and

(c) comparing said test expression level of PAMP polypeptide to a control expression level of PAMP polypeptide,

wherein a test expression level 2-fold or more greater than said control expression level indicates the presence of a prostate neoplastic condition.

22. The method of claim 21, wherein said binding agent selective for said PAMP polypeptide residues 1 to 1074 of SEQ ID NO:2 comprises an antibody.

23. The method of claim 22, wherein said binding agent further comprises a detectable label.

24. A method of diagnosing metastatic prostate cancer in an individual, comprising:

(a) obtaining a sample from said individual, wherein said sample is not a prostate sample;

(b) measuring a test expression level of PAMP RNA by hybridization with a PAMP nucleic acid probe comprising at least 10 contiguous nucleotides of SEQ ID NO:1, said contiguous nucleotides including at least one nucleotide of the nucleotide sequence shown as position 1 to position 3221 of SEQ ID NO:1 in said sample; and

(c) comparing said test expression level of PAMP RNA to a control expression level of PAMP RNA,

wherein a significant test expression level as compared to said control expression level indicates the presence of metastatic prostate cancer.

25. A method of diagnosing metastatic prostate cancer in an individual, comprising:

(a) obtaining a sample from said individual, wherein said sample is not a prostate sample;

(b) measuring a test expression level of PAMP polypeptide by contacting a cell, a cell lysate, or fractionated sample thereof, from said individual with a binding agent selective for PAMP polypeptide residues 1 to 1074 of SEQ ID NO:2, and determining the amount of selective binding of said agent;

(c) comparing said test expression level of PAMP polypeptide to a control expression level of PAMP polypeptide,

wherein a significant test expression level as compared to said control expression level indicates the presence of metastatic prostate cancer.